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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/843,221A

DATE: 03/13/2002
TIME: 11:48:58

Input Set : A:\EP.txt
Output Set: N:\CRF3\03132002\I843221A.raw

3 <110> APPLICANT: KOSTENUIK, PAUL
4 LIU, CHUAN-FA
5 LACEY, DAVID LEE
7 <120> TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

8 RELATED PROTEIN
10 <130> FILE REFERENCE: A-665B
12 <140> CURRENT APPLICATION NUMBER: 09/843,221A
13 <141> CURRENT FILING DATE: 2001-04-26
15 <150> PRIOR APPLICATION NUMBER: 60/266,673
16 <151> PRIOR FILING DATE: 2001-02-06
18 <150> PRIOR APPLICATION NUMBER: 60/214,860
19 <151> PRIOR FILING DATE: 2000-06-28
21 <150> PRIOR APPLICATION NUMBER: 60/200,053
22 <151> PRIOR FILING DATE: 2000-04-27
24 <160> NUMBER OF SEQ ID NOS: 170
26 <170> SOFTWARE: PatentIn version 3.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 684

30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens

33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(684)
36 <223> OTHER INFORMATION:
39 <400> SEQUENCE: 1

40 atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc ctg	48
41 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	
42 1 5 10 15	
44 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	96
45 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
46 20 25 30	
48 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	144
49 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
50 35 40 45	
52 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	192
53 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
54 50 55 60	
56 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	240
57 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
58 65 70 75 80	
60 tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	288
61 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
62 85 90 95	

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64 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc      336
65 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
66      100      105      110
68 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag      384
69 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
70      115      120      125
72 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc      432
73 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
74      130      135      140
76 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
77 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
78 145      150      155      160
80 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
81 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
82      165      170      175
84 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
85 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
86      180      185      190
88 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
89 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
90      195      200      205
92 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
93 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
94      210      215      220
96 tct ccg ggt aaa      684
97 Ser Pro Gly Lys
98 225
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 228
103 <212> TYPE: PRT
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 2
108 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
109 1      5      10      15
112 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
113      20      25      30
116 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
117      35      40      45
120 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
121      50      55      60
124 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
125 65      70      75      80
128 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
129      85      90      95
132 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
133      100      105      110
136 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
137      115      120      125
140 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

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141      130      135      140
144 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 145      150      155      160
148 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
149      165      170      175
152 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
153      180      185      190
156 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
157      195      200      205
160 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
161      210      215      220
164 Ser Pro Gly Lys
165 225
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 21
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: PTH/PTHrP
176 <220> FEATURE:
177 <221> NAME/KEY: misc_feature
178 <222> LOCATION: (1)..(1)
179 <223> OTHER INFORMATION: Optional attachment to X3X4X5X6X7, X2X3X4X5X6X7,
X1X2X3X4X5X6X7
180      , or YX1X2X3X4X5X6X7
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: (1)..(1)
186 <223> OTHER INFORMATION: X8 is an amino acid residue (nonfunctional residue
preferred, M o
187      r Nle most preferred)
190 <220> FEATURE:
191 <221> NAME/KEY: misc_feature
192 <222> LOCATION: (3)..(3)
193 <223> OTHER INFORMATION: X10 is an amino acid residue (an acidic or hydrophilic
residue pr
194      eferred, N or D most preferred)
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: (4)..(4)
200 <223> OTHER INFORMATION: X11 is an amino acid residue (nonfunctional or basic residue
pref
201      erred, L, R, or K most preferred)
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (5)..(5)
207 <223> OTHER INFORMATION: X12 is an amino acid residue (nonfunctional or aromatic
residue p
208      referred, G, F, or W most preferred)
211 <220> FEATURE:
212 <221> NAME/KEY: misc_feature
213 <222> LOCATION: (7)..(7)
214 <223> OTHER INFORMATION: X14 is an amino acid residue (basic or hydrophilic residue

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prefer

215

red, H or S most preferred)

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218 <220> FEATURE:
 219 <221> NAME/KEY: misc_feature
 220 <222> LOCATION: (8)..(8)
 221 <223> OTHER INFORMATION: X15 is an amino acid residue (nonfunctional residue
 preferred, wi
 222 th L or I most preferred)
 225 <220> FEATURE:
 226 <221> NAME/KEY: misc_feature
 227 <222> LOCATION: (9)..(9)
 228 <223> OTHER INFORMATION: X16 is an amino acid residue (nonfunctional or hydrophilic
 residu
 229 e preferred, Q, N, S, or A most preferred)
 232 <220> FEATURE:
 233 <221> NAME/KEY: misc_feature
 234 <222> LOCATION: (10)..(10)
 235 <223> OTHER INFORMATION: X17 is an amino acid residue (acidic, hydrophilic, or
 nonfunction
 236 al residue preferred, S, D, or L most preferred)
 239 <220> FEATURE:
 240 <221> NAME/KEY: misc_feature
 241 <222> LOCATION: (11)..(11)
 242 <223> OTHER INFORMATION: X18 is an amino acid residue (nonfunctional residue
 preferred,M,
 243 L, V or Nle most preferred)
 246 <220> FEATURE:
 247 <221> NAME/KEY: misc_feature
 248 <222> LOCATION: (12)..(12)
 249 <223> OTHER INFORMATION: X19 is an amino acid residue (acidic or basic residue
 preferred,
 250 E or R most preferred)
 253 <220> FEATURE:
 254 <221> NAME/KEY: misc_feature
 255 <222> LOCATION: (14)..(14)
 256 <223> OTHER INFORMATION: X21 is an amino acid residue (nonfunctional residue or basic
 res
 257 idue preferred; V, M, R, or Nle most preferred)
 260 <220> FEATURE:
 261 <221> NAME/KEY: misc_feature
 262 <222> LOCATION: (15)..(15)
 263 <223> OTHER INFORMATION: X22 is an amino acid residue (hydrophilic, acidic, or
 aromatic r
 264 esidue preferred, E or F most preferred)
 267 <220> FEATURE:
 268 <221> NAME/KEY: misc_feature
 269 <222> LOCATION: (16)..(16)
 270 <223> OTHER INFORMATION: X23 is an aromatic or lipophilic residue (W or F preferred)
 273 <220> FEATURE:
 274 <221> NAME/KEY: misc_feature
 275 <222> LOCATION: (17)..(17)
 276 <223> OTHER INFORMATION: X24 is a lipophilic residue (L preferred)
 279 <220> FEATURE:
 280 <221> NAME/KEY: misc_feature
 281 <222> LOCATION: (18)..(18)

282 <223> OTHER INFORMATION: X25 is an amino acid residue (hydrophilic or basic residue
prefe
283 rred, R or H most preferred)
286 <220> FEATURE:

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287 <221> NAME/KEY: misc_feature
288 <222> LOCATION: (19)..(19)
289 <223> OTHER INFORMATION: X26 is an amino acid residue (hydrophilic or basic residue
prefe
290      rred, K or H most preferred)
293 <220> FEATURE:
294 <221> NAME/KEY: misc_feature
295 <222> LOCATION: (20)..(20)
296 <223> OTHER INFORMATION: X27 is an amino acid residue (lipophilic, basic, or
nonfunctiona
297      l residue preferred, K or L most preferred)
300 <220> FEATURE:
301 <221> NAME/KEY: misc_feature
302 <222> LOCATION: (21)..(21)
303 <223> OTHER INFORMATION: X28 is an amino acid residue (lipophilic or nonfunctional
residu
304      e preferred, L or I most preferred)
307 <220> FEATURE:
308 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (21)..(21)
310 <223> OTHER INFORMATION: Optional attachment to X29, X29X30, X29X30X31, X29X30
X31X32, X29
311      X30X31X32X33, X29X30X31X32X33X34, X29X30X31X32X33X34X35, or X29X
312      30X31X32X33X34X35X36
315 <400> SEQUENCE: 3
W--> 317 Xaa His Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
318 1      5      10      15
W--> 321 Xaa Xaa Xaa Xaa Xaa
322      20
325 <210> SEQ ID NO: 4
326 <211> LENGTH: 22
327 <212> TYPE: PRT
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: PTH/PTHrP
333 <220> FEATURE:
334 <221> NAME/KEY: misc_feature
335 <222> LOCATION: (1)..(1)
336 <223> OTHER INFORMATION: Optional attachment to J1J2J3J4J5J6, J2J3J4J5J6, J3J4J5J6
339 <220> FEATURE:
340 <221> NAME/KEY: misc_feature
341 <222> LOCATION: (1)..(1)
342 <223> OTHER INFORMATION: J7 is an amino acid residue (nonfunctional or aromatic
residue pr
343      eferred, L or F most preferred)
346 <220> FEATURE:
347 <221> NAME/KEY: misc_feature
348 <222> LOCATION: (2)..(2)
349 <223> OTHER INFORMATION: J8 is an amino acid residue (nonfunctional residue
preferred, M o
350      r Nle most preferred)
353 <220> FEATURE:
354 <221> NAME/KEY: misc_feature

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355 <222> LOCATION: (6)..(6)

356 <223> OTHER INFORMATION: J12 is an amino acid residue (nonfunctional or aromatic residue p

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF3\03132002\I843221A.raw

L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5